

Qy 1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGAAGTGTGGCCATGGTCCCCAAGACCTCTATAT 1557
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 Db 36621 CCACAGCCCAGGCCTCCAGCTCAGCAGTGAAGTGTGGCCATGGTCCCCAAGACCTCTATAT 36562

Qy 1558 TTGCTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTC 1617
 |||
 Db 36561 TTGCTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTC 36502

Qy 1618 AGGACC 1623
 |||
 Db 36501 AGGACC 36496

SR Guided comparison A

RESULT 3
 HSU32674
 LOCUS HSU32674 1293 bp DNA PRI 05-JUN-1996
 DEFINITION Human orphan receptor GPR9 (GPR9) gene, partial cds.
 ACCESSION U32674
 VERSION U32674.1 GI:1002740
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1293)
 AUTHORS Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,
 Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.
 and Docherty,J.M.
 TITLE Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
 and GPR14, encoding receptors related to interleukin 8,
 neuropeptide Y, and somatostatin receptors
 JOURNAL Genomics 29 (2), 335-344 (1995)
 MEDLINE 96115583

REFERENCE 2 (bases 1 to 1293)
 AUTHORS Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,
 Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.
 and Docherty,J.M.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-1995) B.F. O'Dowd, Department of Pharmacology,
 University of Toronto, 8 Taddle Creek Rd., Toronto, Ontario M5S
 1A8, Canada

FEATURES
 source Location/Qualifiers
 1. .1293
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 gene 1. .1203
 /gene="GPR9"
 CDS <109. .1203
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 is an orphan receptor similar to the interleukin 8
 receptors"
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 /db_xref="GI:1002741"
 /translation="VSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS
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 PLWAVDAAVQWVFGSLCKVAGALFNIFYAGALLACISFDRLNIVHATQLYRRGP
 PARVTLTCLAVWGLCLLPDFIFLSAHHDERLNATHCQYNFPQVGRTRALRVLQVLA
 GFLPLLVMAICYAHILAVLLVSRGQRRRLAMRLVVVVVAFALCWTPYHLVVLVDIL
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BASE COUNT 201 a 458 c 357 g 277 t
 ORIGIN

Qy	58	CCAGCCCGAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG	117
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Qy	118	CCGCCCTCCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGACTCGT	177
Db	146	CCGCCCTCCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGACTCGT	205
Qy	178	GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCTCTGC	237
Db	206	GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCTCTGC	265
Qy	238	CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG	297
Db	266	CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG	325
Qy	298	TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCAGACACCTTCCTGCTCCACCTAGCTG	357
Db	326	TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCAGACACCTTCCTGCTCCACCTAGCTG	385
Qy	358	TAGCAGACACGCTGCTGGTGTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT	417
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Qy	418	GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG	477
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Qy	478	CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGTACCTGAACATAGTTTCATGCCA	537
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Qy	538	CCCAGCTCTACCGCCGGGGGGCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG	597
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Qy	598	GGCTCTGCCTGCTTTTTCGCCCTCCAGACTTCATCTTCTGTGCGGCCACCACGACGAGC	657
Db	626	GGCTCTGCCTGCTTTTTCGCCCTCCAGACTTCATCTTCTGTGCGGCCACCACGACGAGC	685
Qy	658	GCCTCAACGCCACCCACTGCCAATAACAACCTTCCCACAGGTGGGCGCAGCGCTCTGCGGG	717
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Qy	718	TGCTGCAGCTGGTGGCTGGCTTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCC	777
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Qy	778	ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGCGCCTGCGGGCCATGCGGCTGG	837
Db	806	ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGCGCCTGCGGGCCATGCGGCTGG	865
Qy	838	TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGTCTGG	897
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Qy	898	TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG	957
Db	926	TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG	985
Qy	958	ACGTGGCCAAAGTCGGTCACCTCAGGCCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC	1017
Db	986	ACGTGGCCAAAGTCGGTCACCTCAGGCCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC	1045
Qy	1018	TCTATGCCTTTGTAGGGGTCAAGTTCGGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG	1077

Sequence comparison A

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Db      1046 TCTATGCCTTTGTAGGGGTCAAGTTCGCGGAGCGGATGTGGATGCTGCTCTTGC GCCTGG 1105
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Db      1106 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTATCCT 1165
Qy      1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197
Db      1166 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1225
Qy      1198 TCGCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257
Db      1226 TCGCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1285
Qy      1258 CTCCCCAA 1265
Db      1286 CTCCCCAA 1293

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RESULT 1
V26557
ID V26557 standard; DNA; 1670 BP.
XX
AC V26557;
XX
DT 14-AUG-1998 (first entry)
XX
DE Human IP-10/Mig receptor CXCR3 gene.
XX
KW ds; chemokine receptor; cellular signal; treatment; T cell;
KW inflammatory disease; antitumour; antiviral.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 69..1175
FT /*tag= a
FT /product= "IP-10/Mig receptor CXCR3"
FT polyA_signal 1534..1539
FT /*tag= b
FT polyA_site 1624..1670
FT /*tag= c
XX
PN WO9811218-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-US15915.
XX
PR 31-MAR-1997; 97US-0829839.
PR 10-SEP-1996; 96US-0709838.
XX
PA (KOCH-) KOCHER INST THEODOR.
PA (LEUK-) LEUKOSITE INC.
XX
PI Loetscher M, Mackay CR, Moser B, Qin S;
XX
DR WPI; 1998-207381/18.
DR P-PSDB; W54371.
XX
PT DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of
PT which, are useful for treatment of inflammation or in anti-tumour or
PT anti-viral therapy
XX
PS Claim 6; Fig 1; 137pp; English.
XX
CC The mammalian CXC chemokine receptor 3 (CXCR3) gene encodes a protein
CC which can selectively bind one or more chemokines and can mediate
CC cellular signalling and/or a cellular response in response. Inhibitors

```

CC and promoters of mammalian CXCR3 can be detected and identified using
CC host cells expressing CXCR3. CXCR3 inhibitors can be used for treatment
CC of inflammatory diseases which are T cell mediated. CXCR3 promoters are
CC useful for antitumour or antiviral therapy.

XX

SQ Sequence 1670 BP; 272 A; 574 C; 436 G; 388 T; 0 other;

Query Match 100.0%; Score 1670; DB 19; Length 1670;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 GCCCAGCCATGGTCTTGTAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCG 120
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Qy    121 CCCTCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGACTCGTGCT 180
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Db    121 ccctctggagaacttcagctcttctctatgactatggagaaaacgagagtgactcgtgct 180

Qy    181 GTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAAGTTCGACCGGGCCTTCTGCCAG 240
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Qy    301 TGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCTGCTCCACCTAGCTGTAG 360
          |||
Db    301 tgctgagccggcgagacgccctgagcagcaccgacaccttctgctccacctagctgtag 360

Qy    361 CAGACACGCTGCTGGTGTGACTGCGGCTCTGGGAGTGGACGCTGCCGTCCAGTGGG 420
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Db    361 cagacacgctgctggtgctgacactgccgctctgggcagtggacgctgccgtccagtggg 420

Qy    421 TCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAG 480
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Qy    661 TCAACGCCACCCACTGCCAATAACAACCTCCACAGGTGGGCCGCACGGCTCTGCGGGTGC 720
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Db    661 tcaacgccaccactgccaataacaacttcccacaggtgggcccgcacggctctgcggtgc 720

Qy    721 TGCACTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCACACA 780
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Qy    781 TCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGCGCCTGCGGGCCATGCGGCTGGTGG 840
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Qy    841 TGGTGGTCTGCTGGTGGCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGGTGG 900
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```

RN      [2]
RP      SEQUENCE OF 5-368 FROM N.A.
RX      MEDLINE; 96115583.
RA      Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R.,
RA      Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
RA      O'Dowd B.F., Docherty J.M.;
RT      "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
RT      and GPR14, encoding receptors related to interleukin 8, neuropeptide
RT      Y, and somatostatin receptors.";
RL      Genomics 29:335-344(1995).

```

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RN      [3]
RP      LIGAND BINDING.
RC      TISSUE=FETAL ASTROCYTES;
RX      MEDLINE; 98290735.
RA      Cole K.E., Strick C.A., Paradis T.J., Ogborne K.T., Loetscher M.,
RA      Gladue R.P., Lin W., Boyd J.G., Moser B., Wood D.E., Sahagan B.G.,
RA      Neote K.;
RT      "Interferon-inducible T cell alpha chemoattractant (I-TAC): A novel
RT      non-ELR CXC chemokine with potent activity on activated T cells
RT      through selective high affinity binding to CXCR3.";
RL      J. Exp. Med. 187:2009-2021(1998).
CC      -!- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP10 AND SCYB11/ITAC.
CC      -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

```

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DR      EMBL; X95876; CAA65126.1; -.
DR      EMBL; U32674; AAC50505.1; -.
DR      GCRDB; GCR_1341; -.
DR      GCRDB; GCR_1972; -.
DR      MIM; 600894; -.
DR      INTERPRO; IPR000276; -.
DR      PFAM; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRRHODOPSIN.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
FT      DOMAIN          1          53      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        54          80      1 (POTENTIAL).
FT      DOMAIN          81          89      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        90         110      2 (POTENTIAL).
FT      DOMAIN         111         125      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        126         147      3 (POTENTIAL).
FT      DOMAIN         148         169      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        170         189      4 (POTENTIAL).
FT      DOMAIN         190         212      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        213         233      5 (POTENTIAL).
FT      DOMAIN         234         255      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        256         277      6 (POTENTIAL).
FT      DOMAIN         278         298      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        299         321      7 (POTENTIAL).
FT      DOMAIN         322         368      CYTOPLASMIC (POTENTIAL).
FT      DISULFID        124         203      BY SIMILARITY.
FT      CARBOHYD         22          22      N-LINKED (GLCNAC. . .) (POT
FT      CARBOHYD         32          32      N-LINKED (GLCNAC. . .) (POT
SQ      SEQUENCE        368 AA;  40659 MW;  F08A3B44B2BBAD04 CRC64;

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Signature of Commissioner

Query Match 100.0%; Score 1907; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCQDQDFSLNFDRAFLPALY 60
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Db 1 MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCQDQDFSLNFDRAFLPALY 60

Sequenced comparison B

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Db     181 LFLALPDFIFLSAHHDERLNATHCQYNFPQVGR TALRVLQLVAGFLLPLLVMAYCYAHILA 240

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Qy     301 SVTSGLYMHCCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLRQPSRRDSSWSET 360
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Db     301 SVTSGLYMHCCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLRQPSRRDSSWSET 360

Qy     361 SEASYSGL 368
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Db     361 SEASYSGL 368

```

RESULT 4
CCR5_HUMAN

ID CCR5_HUMAN STANDARD; PRT; 372 AA.
AC P32302; Q14811;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXC-R5) (CXCR-5) (BURKITT'S LYMPHOMA
DE RECEPTOR 1) (MONOCYTE-DERIVED RECEPTOR 15) (MDR15).
GN BLR1 OR CXCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A. (LONG FORM).
RC TISSUE=LYMPHOCYTES;
RX MEDLINE; 93049615.
RA Dobner T., Wolf I., Emrich T., Lipp M.;
RT "Differentiation-specific expression of a novel G protein-coupled
RT receptor from Burkitt's lymphoma.";
RL Eur. J. Immunol. 22:2795-2799(1992).
RN [2]
RP SEQUENCE FROM N.A. (SHORT FORM).
RC TISSUE=BLOOD;
RX MEDLINE; 95366951.
RA Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;
RT "Sequence variation of a novel heptahelical leucocyte receptor
RT through alternative transcript formation.";
RL Biochem. J. 309:773-779(1995).
RN [3]
RP LIGAND BINDING.
RX MEDLINE; 98130629.
RA Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,
RA Baggiolini M., Moser B.;
RT "B cell-attracting chemokine 1, a human CXC chemokine expressed in
RT lymphoid tissues, selectively attracts B lymphocytes via
RT BLR1/CXCR5.";
RL J. Exp. Med. 187:655-660(1998).
CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO BLC. BLR1 EXERTS
CC POSSIBLY A REGULATORY FUNCTION IN BURKITT LYMPHOMA (BL)
CC LYMPHOMAGENESIS AND/OR B-CELL DIFFERENTIATION. IT IS A POTENTIAL
CC CANDIDATE FOR CELL-CELL INTERACTION, AND ACTIVATION OF MATURE B-
CC LYMPHOCYTES IN LYMPHATIC TISSUES.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

Qy	245	SRGQRRRLRAMRLVVVVVVA	FALCWT	PPYHLVLVDILMDL	GALARNCGRES	RV	DAKSVTS	304
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Db	249	QRRPQKQKAVRVAILVTS	IFFLCWSPYHIVIFL	DLTLARLKAVD	NTCKLNGSLP	VAITMCE	308	
Qy	305	GLGYMHCCCLNPLLYAF	VGVKFRERMMWMLLL	RLCQPNQRGLQ	RPSSSRDDSS	SWSETSEAS	364	
		:	: :	:		: : :		
Db	309	FLGLAHCCCLNPMLYTF	FAGVKFRSDLSRL	LLTKLGCTGPAS	LQCQLFSPWRR	-SSLSESE	ENAT 367	


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Qy  901 ACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACG 960
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Db  901 acatcctcatggacctgggcgctttggcccgcaactgtggccgagaaagcagggtagacg 960

Qy  961 TGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCT 1020
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 tggccaagtcggtcacctcaggcctgggctacatgcactgctgcctcaaccgctgctct 1020

Qy  1021 ATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGC GCCTGGGCT 1080
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 atgcctttgtaggggtcaagttccgggagcggatgtggatgctgctcttgccgctgggct 1080

Qy  1081 GCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTTCATCCTGGT 1140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 gcccccaaccagagagggctccagaggcagccatcgctcttcccgccgggattcactcctggt 1140

Qy  1141 CTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCTTTTCG 1200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 ctgagacctcagaggcctcctactcgggcttgtgaggccggaatccgggctcccccttctg 1200

Qy  1201 CCCACAGTCTGACTTCCCGCATTCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTC 1260
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 cccacagtctgacttccccgcattccaggctcctccctccctctgccggctctggctctc 1260

Qy  1261 CCCAATATCCTCGCTCCCGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGGGAA 1320
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 cccaataatcctcgctcccggaactcactggcagccccagcaccaccagggtctcccgga 1320

Qy  1321 GCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCC 1380
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 gccaccctcccagctctgaggactgcaccattgctgctccttagctgccaaagccccatcc 1380

Qy  1381 TGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAACTAAACTTC 1440
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 tgccgcccgaggtggctgcctggagccccactgcccttctcatttggaaactaaacttc 1440

Qy  1441 ATCTTCCCCAAGTGCAGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAGCCA 1500
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 atcttccccaaagtgcagggagtacaaggcatggcgtagagggtgctgccccatgaagcca 1500

Qy  1501 CAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATATTTG 1560
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Db  1501 cagcccaggcctccagctcagcagtgactgtggccatgggtccccaaagacctctatatttg 1560

Qy  1561 CTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTCAGG 1620
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 ctcttttattttatgtctaaatcctgctttaaacttttcaataaacaagatcgtcagg 1620

Qy  1621 ACCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1670
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 acctttttttttttttttttttttttttttttttttttttttttttttttttttttt 1670

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RESULT 2

T72800

ID T72800 standard; cDNA; 1876 BP.

XX

AC T72800;

XX

DT 28-SEP-1997 (first entry)

XX

DE Human G-protein chemokine receptor HSATU68 cDNA.

XX

KW HSATU68; G-protein chemokine receptor; 7-transmembrane receptor;

KW signal transduction; gene therapy; diagnosis; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 173..1420

FT /*tag= a
 FT primer_bind complement (173..190)
 FT /*tag= b
 FT primer_bind 1402..1420
 FT /*tag= c
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 PN WO9725340-A1.
 XX
 PD 17-JUL-1997.
 XX
 PF 11-JAN-1996; 96WO-US00499.
 XX
 PR 11-JAN-1996; 96WO-US00499.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Li Y;
 XX
 DR WPI; 1997-372810/34.
 DR P-PSDB; W19780.
 XX
 PT DNA encoding new isolated human G-protein chemokine receptor - used
 PT to develop products for treating, e.g. autoimmune diseases, chronic
 PT infections, allergy, malignancy, inflammation or shock
 XX
 PS Claim 1; Fig 1a-d; 54pp; English.
 XX
 CC A cDNA clone (T72800) codes for a newly identified human G-protein
 CC chemokine receptor (W19780) designated HSATU68. It was identified
 CC in a human genomic library derived from activated T cells. HSATU68
 CC nucleic acids be used to produce HSATU68 in prokaryotic or
 CC eukaryotic host cells, as probes for the detection, screening and
 CC diagnosis of diseases caused by mutations in the HSATU68 gene, and
 CC in the gene therapy of conditions related to underexpression of the
 CC receptor its ligand.
 XX
 SQ Sequence 1876 BP; 343 A; 625 C; 520 G; 388 T; 0 other;

Query Match 92.2%; Score 1540; DB 18; Length 1876;
 Best Local Similarity 99.0%; Pred. No. 6.2e-287;
 Matches 1549; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 58 CCAGCCCAGCCATGGTCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117
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 Db 303 cctccccgttcccgccctcacaggtgagtgaccaccaagtgctaaatgacgccgaggttg 362
 Qy 118 CCGCCCTCCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGAATCGT 177
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 Db 363 ccgccctcctggagaacttcagctcttctctatgactatggagaaaacgagagtgactcgt 422
 Qy 178 GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACCTCGACCGGGCCTTCCTGC 237
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 Db 423 gctgtacctccccgccctgccacaggacttcagcctgaacttcgaccgggccttctgc 482
 Qy 238 CAGCCCTCTACAGCCTCCTCTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297
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 Db 483 cagccctcaacagcctcctcttctgctggggctgctgggcaacggcgcggtggcagccg 542
 Qy 298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCACCTTCCTGCTCCACCTAGCTG 357
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 Db 543 tgctgctgagccggcgagacgccctgagcagcaccgacaccttctgctccacctagctg 602
 Qy 358 TAGCAGACACGCTGCTGGTGTGACTGCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417
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 Db 603 tagcagacacgctgctggtgctgacactgccgctctgggcagtggacgctgccgtccagt 662
 Qy 418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477
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Qy	478	CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA	537
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Qy	538	CCCAGCTCTACCGCCGGGGCCCCCGGCCCGCTGACCTCACCTGCCTGGCTGTCTGGG	597
Db	783	cccagctctaccgcccggggccccggccgctgaccctcacctgcctggctgtctggg	842
Qy	598	GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCACCACGACGAGC	657
Db	843	ggctctgctgcttttcgccctcccagacttcattctcctgtcggcccaccacgacgagc	902
Qy	658	GCCTCAACGCCACCCACTGCCAATAACAATTCCACAGGTGGGCCGACGGCTCTGCGGG	717
Db	903	gcctcaacgcccaccactgccaataacaattccacaggtgggcccacggctctgcggg	962
Qy	718	TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCTGCTGGTCATGGCTACTGCTATGCCC	777
Db	963	tgctgcagctggtggctggctttctgctgcccctgctggtcatggcctactgctatgccc	1022
Qy	778	ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGCGCCTGCGGGCCATGCGGCTGG	837
Db	1023	acatcctggccgtgctgctggtttccaggggcccagcgcgctgcgggcccagcggtgg	1082
Qy	838	TGGTGGTGGTCGTGGTGGCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGGCTGG	897
Db	1083	tggtggtggtcgtggtggcctttgccctctgctggaccccctatcacctggtggtgctgg	1142
Qy	898	TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG	957
Db	1143	tggaacatcctcatggacctggcgctttggcccgaactgtggccgagaaagcagggtag	1202
Qy	958	ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC	1017
Db	1203	acgtggccaagtcgggtcacctcaggcctgggtacatgcactgctgcctcaaccgctgc	1262
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Qy	1078	GCTGCCCCAACCCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTATCCT	1137
Db	1323	gctgcccacaccagagagggtccagaggcagccatcgctctcccgccgggattcactct	1382
Qy	1138	GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGAATCCGGGCTCCCTT	1197
Db	1383	ggtctgagacctcagaggcctcctactcgggcttgtgaggccggaatccgggctcccctt	1442
Qy	1198	TCGCCCACAGTCTGACTTCCCCGATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT	1257
Db	1443	tcgcccacagtctgacttcccgcattccaggctcctccctccctctgccggctctggct	1502
Qy	1258	CTCCCCAATATCCTCGCTCCCGGACTCACTGGCAGCCCCAGCACCACAGGTCTCCCGG	1317
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Qy	1318	GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA	1377
Db	1563	gaagccaccctcccagctctgaggactgcaccattgctgctccttagctgccaaagcccc	1622
Qy	1378	TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAC	1437
Db	1623	tcctgcccggcgagggtggctgcctggagccccactgcccttctcatttggaactaaaac	1682
Qy	1438	TTCATCTTCCCCAAGTGCGGGAGTACAAGGCATGGCGTAGAGGGTGTGCCCATGAAG	1497
Db	1683	ttcatcttccccaagtgccgggagtaacaaggcatggcgtagagggtgctgccccatgaag	1742
Qy	1498	CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT	1557
Db	1743	ccacagcccaggcctccagctcagcagtgactgtggccatggtccccaagacctctatat	1802

Qy 1558 TTGCTCTTTTATTTTATGTCTAAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTC 1617
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Db 1803 ttggctcttttatttttatgtctaaaatcctgcttaaaacttttcaataaacaagatcgtc 1862

Qy 1618 AGGA 1621
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Db 1863 agga 1866

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RESULT 1
HSGPCRIN8
LOCUS HSGPCRIN8 1670 bp mRNA PRI 16-MAY-1997
DEFINITION H.sapiens mRNA for G-protein coupled receptor.
ACCESSION X95876
VERSION X95876.1 GI:1552845
KEYWORDS G protein-coupled receptor; interleukin-8 receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1670)
AUTHORS Loetscher,M., Gerber,B., Loetscher,P., Jones,S.A., Piali,L.,
Clark-Lewis,I., Baggiolini,M. and Moser,B.
TITLE Chemokine receptor specific for IP10 and mig: structure, function,
and expression in activated T-lymphocytes
JOURNAL J. Exp. Med. 184 (3), 963-969 (1996)
MEDLINE 97188912
REFERENCE 2 (bases 1 to 1670)
AUTHORS Loetscher,M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1996) M. Loetscher, Theodor-Kocher Institute,
University of Bern, Freiestrasse 1, CH-3012 Bern, SWITZERLAND
FEATURES
source Location/Qualifiers
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69. .1175
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/db_xref="SWISS-PROT:P49682"
/translation="MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCP
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RRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVL
QLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRRLAMRLVVVVVAFALCWTPYHLVVL
VDILMDLGALARNCGRESRVDVAKSVTSLGLGYMHCCNLPLLYAFVGVKFRERMWMLL
RLGCPNQRGLRQRPSSSRRDSSWSETSEASYSGL"
polyA_signal 1602. .1607
polyA_site 1623
BASE COUNT 319 a 574 c 436 g 341 t
ORIGIN

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Query Match 97.2%; Score 1623; DB 66; Length 1670;
Best Local Similarity 100.0%; Pred. No. 1.e-255;
Matches 1623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCAACCACAAGCACCAAAGCAGAGGGGCAGGCAGCACACCACCCAGCAGCCAGAGCACCA	60
Db	1	CCAACCACAAGCACCAAAGCAGAGGGGCAGGCAGCACACCACCCAGCAGCCAGAGCACCA	60
Qy	61	GCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCG	120
Db	61	GCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCG	120
Qy	121	CCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCT	180
Db	121	CCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCT	180
Qy	181	GTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAG	240

Db 181 GTACCTCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAG 240

Qy 241 CCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGGGTGGCAGCCGTGC 300
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Db 241 CCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGGGTGGCAGCCGTGC 300

Qy 301 TGCTGAGCCGGCGGACAGCCCTGAGCAGCACCACCTTCCTGCTCCACCTAGCTGTAG 360
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Db 301 TGCTGAGCCGGCGGACAGCCCTGAGCAGCACCACCTTCCTGCTCCACCTAGCTGTAG 360

Qy 361 CAGACACGCTGCTGGTGTGACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGG 420
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Db 361 CAGACACGCTGCTGGTGTGACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGG 420

Qy 421 TCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAG 480
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Db 421 TCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAG 480

Qy 481 GAGCCCTCCTGTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGCCACCC 540
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Db 481 GAGCCCTCCTGTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGCCACCC 540

Qy 541 AGCTCTACCGCCGGGGGCCCCGGCCCGCTGACCCCTACCTGCCTGGCTGTCTGGGGGC 600
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Db 541 AGCTCTACCGCCGGGGGCCCCGGCCCGCTGACCCCTACCTGCCTGGCTGTCTGGGGGC 600

Qy 601 TCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCTGTGCGCCACACGACGAGCGCC 660
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Db 601 TCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCTGTGCGCCACACGACGAGCGCC 660

Qy 661 TCAACGCCACCCACTGCCAATACAACCTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGC 720
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Db 661 TCAACGCCACCCACTGCCAATACAACCTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGC 720

Qy 721 TGCAGCTGGTGGCTGGCTTTCTGCTGCCCTGCTGGTCATGGCCTACTGCTATGCCCACA 780
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Db 721 TGCAGCTGGTGGCTGGCTTTCTGCTGCCCTGCTGGTCATGGCCTACTGCTATGCCCACA 780

Qy 781 TCCTGGCCGTGTGCTGGTTTCCAGGGGCCAGCGGCCCTGCGGGCCATGCGGCTGGTGG 840
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Db 781 TCCTGGCCGTGTGCTGGTTTCCAGGGGCCAGCGGCCCTGCGGGCCATGCGGCTGGTGG 840

Qy 841 TGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGTGGTGG 900
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Db 841 TGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGTGGTGG 900

Qy 901 ACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACG 960
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Db 901 ACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACG 960

Qy 961 TGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCT 1020
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Db 961 TGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCT 1020

Qy 1021 ATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCT 1080
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Db 1021 ATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCT 1080

Qy 1081 GCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGT 1140
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Db 1081 GCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGT 1140

Qy 1141 CTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGAATCCGGGCTCCCCTTTCG 1200
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Db 1141 CTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGAATCCGGGCTCCCCTTTCG 1200

Qy 1201 CCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTC 1260
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Db 1201 CCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTC 1260

Qy 1261 CCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGGGAA 1320

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Db 1261 CCCAATATCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACACCAGGTCTCCCGGGAA 1320
Qy 1321 GCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCC 1380
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Db 1321 GCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCC 1380
Qy 1381 TGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTGGAAACTAAACTTC 1440
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Db 1381 TGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTGGAAACTAAACTTC 1440
Qy 1441 ATCTTCCCCAAGTGCAGGGAGTACAAGGCATGGCGTAGAGGGTGTGCCCCATGAAGCCA 1500
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Db 1441 ATCTTCCCCAAGTGCAGGGAGTACAAGGCATGGCGTAGAGGGTGTGCCCCATGAAGCCA 1500
Qy 1501 CAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATATTG 1560
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Db 1501 CAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATATTG 1560
Qy 1561 CTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAACAAGATCGTCAGG 1620
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Db 1561 CTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAACAAGATCGTCAGG 1620
Qy 1621 ACC 1623
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Db 1621 ACC 1623

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RESULT 2

HSXDP_4/c

WPCOMMENT

Sequence split into 6 fragments LOCUS HSXDP Accession AJ239319

Fragment Name	Begin	End
HSXDP_0	1	110000
HSXDP_1	100001	210000
HSXDP_2	200001	310000
HSXDP_3	300001	410000
HSXDP_4	400001	510000
HSXDP_5	500001	547722

Continuation (5 of 6) of HSXDP from base 400001 (AJ239319 Homo sapiens chromosome X clone cosmid cosE3 map Xq13.1, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces. 5/2000)

Query Match 92.5%; Score 1545.2; DB 90; Length 110000;
 Best Local Similarity 99.2%; Pred. No. 3e-243;
 Matches 1553; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177
      |||
Db 38001 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 37942
Qy 178 GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237
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Db 37941 GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 37882
Qy 238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297
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Db 37881 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 37822
Qy 298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCACACCTTCCTGCTCCACCTAGCTG 357
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Db 37821 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCACACCTTCCTGCTCCACCTAGCTG 37762
Qy 358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417
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Db 37761 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 37702

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Qy 418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477
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 Db 37701 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 37642

Qy 478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537
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 Db 37641 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 37582

Qy 538 CCCAGCTCTACCGCCGGGGGCCCCGGCCCGCTGACCCCTACCTGCCTGGCTGTCTGGG 597
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Qy 958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017
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 Db 37161 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 37102

Qy 1018 TCTATGCCTTTGTAGGGGTCAAGTTCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077
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 Db 37101 TCTATGCCTTTGTAGGGGTCAAGTTCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 37042

Qy 1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTATCCT 1137
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Qy 1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGAATCCGGGCTCCCCTT 1197
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Qy 1198 TCGCCACAGTCTGACTTCCCCGATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257
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 Db 36921 TCGCCACAGTCTGACTTCCCCGATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 36862

Qy 1258 CTCCCCAATATCCTCGCTCCCGGACTCACTGGCAGCCCCAGCACCACAGGTCTCCCGG 1317
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Qy 1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377
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Qy 1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAACTAAAAC 1437
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 Db 36741 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAACTAAAAC 36682

Qy 1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497
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07607186

SLQ ID no: 2

RESULT 1
W54371
ID W54371 standard; Protein; 368 AA.
XX
AC W54371;
XX
DT 14-AUG-1998 (first entry)
XX
DE Human IP-10/Mig receptor CXCR3 protein.
XX
KW chemokine receptor; cellular signal; treatment; T cell; antitumour;
KW antiviral; inflammatory disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /note= "N-linked glycosylation site"
FT Modified-site 32
FT /note= "N-linked glycosylation site"
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FT /note= "TM2 transmembrane domain"
FT Domain 127..147
FT /note= "TM3 transmembrane domain"
FT Domain 170..190
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FT Domain 302..322
FT /note= "TM7 transmembrane domain"
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XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-US15915.
XX
PR 31-MAR-1997; 97US-0829839.
PR 10-SEP-1996; 96US-0709838.
XX
PA (KOCH-) KOCHER INST THEODOR.
PA (LEUK-) LEUKOSITE INC.
XX
PI Loetscher M, Mackay CR, Moser B, Qin S;
XX
DR WPI; 1998-207381/18.
DR N-PSDB; V26557.
XX
PT DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of
PT which, are useful for treatment of inflammation or in anti-tumour or
PT anti-viral therapy
XX
PS Claim 7; Fig 2; 137pp; English.
XX
CC The mammalian CXC chemokine receptor 3 (CXCR3) protein can selectively
CC bind one or more chemokines and can mediate cellular signalling and/or a
CC cellular response in response. Inhibitors and promoters of mammalian
CC CXCR3 can be detected and identified using host cells expressing CXCR3.
CC CXCR3 inhibitors can be used for treatment of inflammatory diseases which
CC are T cell mediated. CXCR3 promoters are useful for antitumour or
CC antiviral therapy.
XX
SQ Sequence 368 AA;

Query Match 100.0%; Score 1907; DB 19; Length 368;
 Best Local Similarity 100.0%; Pred. No. 1.6e-217;
 Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MVLEVS DHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPDQFSLNFDRAFLPALY 60
      |||
Db      1 mvlevsdhqvlndaevaallenfsssydygenesdscctspcpqdfslnfdraflpaly 60

Qy     61 SLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLVLVTLPLWAVDAAVQWVFG 120
      |||
Db     61 slflglilgngavaavllsrrtalsstdtfllhlavadtllvltlplwavdaavqwvfg 120

Qy    121 SGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCL 180
      |||
Db    121 sgckvagalfninfyagalllacisfdrylnivhatqlyrrgpparvlttclavwglcl 180

Qy    181 LFALPDFIFLSAHHDERLNATHCQYNFPQVGR TALRVLQLVAGFLLPLLVMAYCYAHILA 240
      |||
Db    181 lfalpdfiflsahhderlnathcqynfpqvg rtalrvlqlvagfllpllvmaycyahila 240

Qy    241 VLLVSRGQRRLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAK 300
      |||
Db    241 vllvsrgqr rramrlvvvvvafalcwtpyhlvvlvdilmdlgalarncgresrvdvak 300

Qy    301 SVTSGLG YMHCCLNPLLYAFVG VKFRERMWMLLLRLGCPNQRGLQRPSSSRDSSWSET 360
      |||
Db    301 svtsglgy mhcclnpllyafvgvkfrermwml lrlgcpnqr glrqps srrdsswset 360

Qy    361 SEASYSGL 368
      |||
Db    361 seasysgl 368
  
```

RESULT 6

R27793

ID R27793 standard; Protein; 372 AA.

XX

AC R27793;

XX

DT 12-MAR-1993 (first entry)

XX

DE New platelet factor 4 receptor superfamily member PF4ARii.

XX

KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;

KW pro-inflammatory cytokine; 8rr.9.

XX

OS Homo sapiens.

XX

PN WO9217497-A.

XX

PD 15-OCT-1992.

XX

PF 23-MAR-1992; 92WO-US02317.

XX

PR 29-MAR-1991; 91US-0677211.

PR 19-DEC-1991; 91US-0810782.

XX

PA (GETH) GENENTECH INC.

XX

PI Holmes WE, Lee J, Wood WI;

XX

DR WPI; 1992-366191/44.

DR N-PSDB; Q37107.

XX

PT Isolated human platelet factor 4 super-family receptor

PT polypeptide and corresp. antibodies and DNA - useful as

PT diagnostic and screening agents, and for treating inflammation or

PT PF4AR-mediated disorders

XX

A;Molecule type: mRNA
A;Residues: 151-269 <WIL>
A;Cross-references: GB:L20332; NID:g438798; PIDN:AAA16852.1; PID:g438799
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.6%; Score 640; DB 2; Length 374;
Best Local Similarity 40.9%; Pred. No. 3.5e-50;
Matches 143; Conservative 54; Mismatches 139; Indels 14; Gaps 6;

Qy	23	FSSSYDYGENESDSCCTSPPCQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR	82
		: : : : : : : : : : :	
Db	26	YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSILFLLGMMGNILVLVILERHR	82
Qy	83	TALSSTDTFLLHLAVADTLLVLTPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL	142
		: : : : : : :	
Db	83	HTRSSTETFLFHLAVADLLVLFILPFAVAEGSVGVWLTFLCKTVIALHKINIFYCSSLLV	142
Qy	143	ACISFDRLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFPDFIFLSA---HHDERLN	199
		: : : : : : :	
Db	143	ACIAVDRLAIVHAVHAYRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDL-	201
Qy	200	ATHCQYNFPQVGRT---ALRVLQVLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRRLAM	254
		: : : : : : : :	
Db	202	-PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLQAQRRPQRQKAV	260
Qy	255	RLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN	314
		: : : : : :	
Db	261	RVAILVTSIFFLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN	320
Qy	315	PLLYAFYGVKFRERMWMLLLRLGCPNQRGLQRQPSSRRDSSWSETSEAS	364
		: : : :	
Db	321	PMLYTFAGVKFRSDLSRLLTCLGCAGPASL-CQLFPNWRKSSLSESEENAT	369

RESULT 5
A53611
interleukin-8 receptor type B - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: I37898; I38712; A53611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptors A and B.
A;Reference number: I37898; MUID:95014476
A;Accession: I37898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803
A;Accession: I38712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
A;Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873;
NID:g511810; PID:g511811; EMBL:U11874; NID:g511812; PID:g511813; EMBL:U11875;
NID:g511814; PID:g511815; EMBL:U11876; NID:g511816; PID:g511817; EMBL:U11877;
NID:g511818; PID:g511819; EMBL:U11878; NID:g511820; PID:g511821
R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A;Title: Structure, genomic organization, and expression of the human interleukin-8 receptor B gene.
A;Reference number: A53611; MUID:94209273
A;Accession: A53611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 6-360 <SPR>

A;Cross-references: GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A;Reference number: A39446; MUID:91368200
A;Accession: A39446
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 6-360 <MUR>
A;Cross-references: GB:M73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, including GRO, NAP-2, and ENA-78.
C;Genetics:
A;Gene: GDB:IL8RB; IL8RA
A;Cross-references: GDB:127868; OMIM:146928
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.2%; Score 633; DB 2; Length 360;
Best Local Similarity 40.1%; Pred. No. 1.4e-49;
Matches 141; Conservative 51; Mismatches 130; Indels 30; Gaps 6;

Qy	25	SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA	84
		: : : :: : :: :	
Db	21	SNYSYSSTLPPFLDAAPEPE-SLEINKYFVVIYALVFLSLGNSLVMVLVILYSRVG	79
Qy	85	LSSTDTFLLHLAVADTLLVLTPLWAVDAVQWVFGSGLCKVAGALFNINFYAGALLLAC	144
		: : :	
Db	80	RSVTDVYLLNLALADLLFALTLPWAASKVNGWIFGTFLCKVVSLKEVNFYSGILLLAC	139
Qy	145	ISFDRYLNIHVHATQLYRRGPPARVTLT-----CLAVWGLCLLFALPDFIFLSAHH	195
		:	
Db	140	ISVDRYLAIVHATR-----TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS	189
Qy	196	ERLNATHCQYNFPQVG-----RTALRVLQVLVAGFLLPLLVMAYCYAHILAVLLVSRGQR	249
		: : : : : :	
Db	190	SNVSPA-C---YEDMGNNNTANWRMLLRILPQSFGFIVPLLIMLCYGFTRLTLFKAHMGQ	245
Qy	250	RLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLG	309
		: :	
Db	246	KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVQETCERRNHIDRALDATEILGIL	305
Qy	310	HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRDSSWSETS	361
		: :	
Db	306	HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPRKDSRPSFVGSSSGHTS	357

RESULT 1
CCR3_HUMAN
ID CCR3_HUMAN STANDARD; PRT; 368 AA.
AC P49682;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 3 (CXC-R3) (CXCR-3).
GN CXCR3 OR GPR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE; 97188912.
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L.,
RA Clark-Lewis I., Baggiolini M., Moser B.;
RT "Chemokine receptor specific for IP10 and mig: structure, function,
RT and expression in activated T-lymphocytes."
RL J. Exp. Med. 184:963-969(1996).